

## SEQUENCE LISTING

<110> Sprecher, Cindy A.  
 Novak, Julia E.  
 West, James W.  
 Presnell, Scott R.  
 Holly, Richard D.  
 Nelson, Andrew J.

<120> SOLUBLE ZALPHA11 CYTOKINE RECEPTORS

<130> 00-22

<150> US 60/194,731

<151> 2000-04-05

<150> US 60/222,121

<151> 2000-07-28

<160> 86

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1614)

<400> 1

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ggc	tgg	ggc	tgc	ccc	gac	ctc	gtc	tgc	tac	acc	gat	tac	ctc	cag	acg	96
Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr	
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gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	cac	ccc	agc	acg	ctc	acc	144

Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr	
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ctt	acc	tgg	caa	gac	cag	tat	gaa	gag	ctg	aag	gac	gag	gcc	acc	tcc	192
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	
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tgc	agc	ctc	cac	agg	tgc	gcc	cac	aat	gcc	acg	cat	gcc	acc	tac	acc	240
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	
		65			70					75					80	
tgc	cac	atg	gat	gta	ttc	cac	ttc	atg	gcc	gac	gac	att	ttc	agt	gtc	288
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	
				85					90					95		
aac	atc	aca	gac	cag	tct	ggc	aac	tac	tcc	cag	gag	tgt	ggc	agc	ttt	336
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	
			100					105					110			
ctc	ctg	gct	gag	agc	atc	aag	ccg	gct	ccc	cct	ttc	aac	gtg	act	gtg	384
Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val	
			115				120					125				
acc	ttc	tca	gga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	432
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	
		130				135					140					
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Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	
		145			150				155					160		
agg	aac	cgg	gga	gac	ccc	tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc	528
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	
			165					170						175		
tca	gtg	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	ctg	gag	ttc	cgc	aaa	576
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys	
			180					185					190			
gac	tgc	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	ccc	atg	cct	ggc	tcc	624
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser	
			195				200					205				

tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln 210 215 220	672
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu 225 230 235 240	720
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acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser 260 265 270	816
cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe 275 280 285	864
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ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His 305 310 315 320	960
cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu 325 330 335	1008
cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp 340 345 350	1056
ccg aca gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp 355 360 365	1104
cgg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala 370 375 380	1152

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cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser 420 425 430	1296
gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg 435 440 445	1344
cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro 450 455 460	1392
tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser 465 470 475 480	1440
ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly 485 490 495	1488
tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp 500 505 510	1536
gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro 515 520 525	1584
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&lt;210&gt; 2

&lt;211&gt; 538

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr  
 20 25 30  
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr  
 35 40 45  
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser  
 50 55 60  
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr  
 65 70 75 80  
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val  
 85 90 95  
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe  
 100 105 110  
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val  
 115 120 125  
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp  
 130 135 140  
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr  
 145 150 155 160  
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile  
 165 170 175  
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys  
 180 185 190  
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser  
 195 200 205  
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln  
 210 215 220  
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu  
 225 230 235 240  
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys  
 245 250 255  
 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser  
 260 265 270  
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe  
 275 280 285  
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly  
 290 295 300

Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His  
 305 310 315 320  
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu  
 325 330 335  
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp  
 340 345 350  
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp  
 355 360 365  
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala  
 370 375 380  
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro  
 385 390 395 400  
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp  
 405 410 415  
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser  
 420 425 430  
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg  
 435 440 445  
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro  
 450 455 460  
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser  
 465 470 475 480  
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly  
 485 490 495  
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp  
 500 505 510  
 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro  
 515 520 525  
 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser  
 530 535

&lt;210&gt; 3

&lt;211&gt; 696

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(696)

&lt;400&gt; 3

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gat	ttc	ttc	ctg	acc	act	atg	ccc	act	gac	tcc	ctc	agt	gtt	tcc	act	96
Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp	Ser	Leu	Ser	Val	Ser	Thr	
			20					25					30			
ctg	ccc	ctc	cca	gag	gtt	cag	tgt	ttt	gtg	ttc	aat	gtc	gag	tac	atg	144
Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val	Phe	Asn	Val	Glu	Tyr	Met	
		35				40					45					
aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	cag	cct	acc	aac	ctc	act	192
Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro	Gln	Pro	Thr	Asn	Leu	Thr	
		50				55					60					
ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	gat	aaa	gtc	cag	aag	tgc	240
Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn	Asp	Lys	Val	Gln	Lys	Cys	
	65				70				75					80		
agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	tct	ggc	tgt	cag	ttg	caa	288
Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr	Ser	Gly	Cys	Gln	Leu	Gln	
			85					90					95			
aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	gtt	gtt	cag	ctc	cag	gac	336
Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe	Val	Val	Gln	Leu	Gln	Asp	
		100					105					110				
cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	atg	cta	aaa	ctg	cag	aat	384
Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln	Met	Leu	Lys	Leu	Gln	Asn	
		115				120					125					
ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	aca	ctt	cac	aaa	ctg	agt	432
Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu	Thr	Leu	His	Lys	Leu	Ser	
	130				135					140						
gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	aga	ttc	ttg	aac	cac	tgt	480
Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn	Arg	Phe	Leu	Asn	His	Cys	
	145			150				155					160			
ttg	gag	cac	ttg	gtg	cag	tac	cgg	act	gac	tgg	gac	cac	agc	tgg	act	528
Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp	Trp	Asp	His	Ser	Trp	Thr	
			165				170						175			

gaa caa tca gtg gat tat aga cat aag ttc tcc ttg cct agt gtg gat 576  
 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp  
 180 185 190

ggg cag aaa cgc tac acg ttt cgt gtt cgg agc cgc ttt aac cca ctc 624  
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu  
 195 200 205

tgt gga agt gct cag cat tgg agt gaa tgg agc cac cca atc cac tgg 672  
 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp  
 210 215 220

ggg agc aat act tca aaa gag aat 696  
 Gly Ser Asn Thr Ser Lys Glu Asn  
 225 230

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 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 4

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 Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met  
 35 40 45  
 Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr  
 50 55 60  
 Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys  
 65 70 75 80  
 Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln  
 85 90 95  
 Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp  
 100 105 110  
 Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn  
 115 120 125  
 Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser  
 130 135 140  
 Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys  
 145 150 155 160



Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr  
                             165                            170                            175  
 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp  
                             180                            185                            190  
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu  
                             195                            200                            205  
 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp  
                             210                            215                            220  
 Gly Ser Asn Thr Ser Lys Glu Asn  
 225                            230

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 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(654)

<400> 5

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atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc ctt acc tgg 96  
 Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp  
                             20                            25                            30

caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc 144  
 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu  
                             35                            40                            45

cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg 192  
 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met  
                             50                            55                            60

gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca 240  
 Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr  
                             65                            70                            75                            80

gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct 288

Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala  
85 90 95

gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca 336  
Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser  
100 105 110

gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc 384  
Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe  
115 120 125

tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg 432  
Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg  
130 135 140

gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac 480  
Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp  
145 150 155 160

tca aga agt gtc tcc ctg ctc ccc ctg gag ttc cgc aaa gac tgg agc 528  
Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser  
165 170 175

tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag 576  
Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln  
180 185 190

ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca 624  
Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser  
195 200 205

gag gag tta aag gaa ggc tgg aac cct cac 654  
Glu Glu Leu Lys Glu Gly Trp Asn Pro His  
210 215

&lt;210&gt; 6

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys  
1 5 10 15

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Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
      20      25      30
Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
      35      40      45
His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
      50      55      60
Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
      65      70      75      80
Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
      85      90      95
Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser
      100      105      110
Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe
      115      120      125
Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg
      130      135      140
Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp
      145      150      155      160
Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser
      165      170      175
Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln
      180      185      190
Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser
      195      200      205
Glu Glu Leu Lys Glu Gly Trp Asn Pro His
      210      215

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<210> 7

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of soluble  
 zalphall Receptor polypeptide as shown in SEQ ID  
 NO:6

<221> misc\_feature

<222> (1)..(654)

<223> n = A,T,C or G

&lt;400&gt; 7

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tggaayytnc	ayccnwsnac	nytnacnytn	acntggcarg	aycartayga	rgarytnaar	120
gaygargcna	cnwsntgyws	nytncaymgn	wsngcncaya	aygcnaacna	ygcnacntay	180
acntgycaya	tggaagtntt	ycayttyatg	gcngaygaya	thttywsgnt	naayathacn	240
gaycarwsng	gnaaytayws	ncargartgy	ggwnsnttyy	tnytngcnga	rwsnathaar	300
ccngcncnc	cnttyaaygt	nacngtnacn	ttysnggnc	artayaayat	hwsntggmgn	360
wsngaytayg	argayccngc	nttytayatg	ytnaarggna	arytncarta	ygarytncar	420
taymgnaaym	gnggngaycc	ntgggcngtn	wsnccnmgnm	gnaarytnat	hwsngtngay	480
wsnmgnwsng	tnwsnytnyt	nccnytngar	ttymgnaarg	aywsnwsnta	ygarytncar	540
gtnmngcng	gnccnatgcc	nggnwsnwsn	taycarggna	cntggwsnga	rtggwsngay	600
ccngtnatht	tycaracnca	rwsngargar	ytnaargarg	gntggaaycc	ncay	654

&lt;210&gt; 8

&lt;211&gt; 696

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Degenerate polynucleotide sequence of IL-2R $\gamma$ ma  
polypeptide as shown in SEQ ID NO:4

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(696)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 8

ytnaayacna	cnathytnac	nccnaayggn	aaygargaya	cnacngcnga	yttyttyytn	60
acnacnatgc	cnacngayws	nytnwsngtn	wsnacnytn	cnytnccnga	rgtncartgy	120
ttgytnttya	aygtngarta	yatgaaytg	acntggaayw	snwsnwsnga	rcncarcncc	180
acnaayytna	cnytncayta	ytggtayaar	aaywsngaya	aygayaargt	ncaraartgy	240
wsncaytayy	tnttywsnga	rgarathacn	wsngngtgy	arytncaraa	raargarath	300
cayytntygc	aracnttygt	ngtnrcarytn	cargayccnm	gngarccnmg	nmgncargcn	360
acncaratgy	tnaarytnca	raayytngtn	athccntggg	cncncgaraa	yytnacnytn	420
cayaarytnw	sngarwsnca	rytngarytn	aaytggaaya	aymgnttyt	naaycaytg	480
ytngarcayy	tngtncarta	ymgnacngay	tgggaycayw	sntggacnga	rcarwsngtn	540
gaytaymgnc	ayaarttyws	nytnccnwsn	gtngayggnc	araarmgnta	yacnttymg	600
gtnmgnwsnm	gnttyaaycc	nytnngygg	wsngcncarc	aytggswnga	rtggwsnca	660
ccnathcayt	gggnwsnaa	yacnwsnaar	garaay			696

&lt;210&gt; 9

&lt;211&gt; 486

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(486)

<400> 9

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Met Arg Ser Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met	
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gtc atc ttc ttg ggg aca ctg gtc cac aaa tca agc tcc caa ggt caa	96
Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln	
20 25 30	
gat cgc cac atg att aga atg cgt caa ctt ata gat att gtt gat cag	144
Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln	
35 40 45	
ctg aaa aat tat gtg aat gac ttg gtc cct gaa ttt ctg cca gct cca	192
Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro	
50 55 60	
gaa gat gta gag aca aac tgt gag tgg tca gct ttt tcc tgt ttt cag	240
Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln	
65 70 75 80	
aag gcc caa cta aag tca gca aat aca gga aac aat gaa agg ata atc	288
Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile	
85 90 95	
aat gta tca att aaa aag ctg aag agg aaa cca cct tcc aca aat gca	336
Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala	
100 105 110	
ggg aga aga cag aaa cac aga cta aca tgc cct tca tgt gat tct tat	384
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr	
115 120 125	
gag aaa aaa cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc	432
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu	
130 135 140	

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<210> 10
<211> 162
<212> PRT
<213> Homo sapiens
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<210> 11  
<211> 1735  
<212> DNA  
<213> mus musculus

<220>  
<221> CDS

&lt;222&gt; (143)...(1729)

&lt;400&gt; 11

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cgcccaggag accacccaag tgcccagcc taaagaatgg ctttctgaga aagaccctga	120
aggagtaggt ctgggacaca gc atg ccc cgg ggc cca gtg gct gcc tta ctc	172
Met Pro Arg Gly Pro Val Ala Ala Leu Leu	
1 5 10	
ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act tgc tac	220
Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr	
15 20 25	
act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc	268
Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg Ser Pro	
30 35 40	
aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag gaa ctt	316
Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu	
45 50 55	
cag gac caa gag acc ttc tgc agc cta cac agg tct ggc cac aac acc	364
Gln Asp Gln Glu Thr Phe Cys Ser Leu His Arg Ser Gly His Asn Thr	
60 65 70	
aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc ctg tcc	412
Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe Leu Ser	
75 80 85 90	
gat gaa gtt ttc att gtc aat gtg acg gac cag tct ggc aac aac tcc	460
Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn Asn Ser	
95 100 105	
caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aaa cca gct ccc	508
Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro Ala Pro	
110 115 120	
ccc ttg aac gtg act gtg gcc ttc tca gga cgc tat gat atc tcc tgg	556
Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp	
125 130 135	
gac tca gct tat gac gaa ccc tcc aac tac gtg ctg agg ggc aag cta	604

Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu			
140	145	150	
caa tat gag ctg cag tat cgg aac ctc aga gac ccc tat gct gtg agg	652		
Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg			
155	160	165	170
ccg gtg acc aag ctg atc tca gtg gac tca aga aac gtc tct ctt ctc	700		
Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser Leu Leu			
	175	180	185
cct gaa gag ttc cac aaa gat tct agc tac cag ctg cag gtg cgg gca	748		
Pro Glu Glu Phe His Lys Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala			
	190	195	200
gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag tgg agt	796		
Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser			
	205	210	215
gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca ggc tgg	844		
Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp			
	220	225	230
gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc ctg gtt	892		
Asp Pro His Met Leu Leu Leu Ala Val Leu Ile Ile Val Leu Val			
	235	240	245
ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa aag ata	940		
Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys Lys Ile			
	255	260	265
tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg tac agg	988		
Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg			
	270	275	280
gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc acg gcc	1036		
Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe Thr Ala			
	285	290	295
tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca gcc tta	1084		
Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu			
	300	305	310



cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg ctg ccg His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro 315 320 325 330	1132
ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct ggt cac Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro Gly His 335 340 345	1180
tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc tac agt Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser 350 355 360	1228
gag gag aga gac cgg cca tat ggt ctg gtg tcc att gac aca gtg act Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr 365 370 375	1276
gtg gga gat gca gag ggc ctg tgt gtc tgg ccc tgt agc tgt gag gat Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys Glu Asp 380 385 390	1324
gat ggc tat cca gcc atg aac ctg gat gct ggc cga gag tct ggc cct Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro 395 400 405 410	1372
aat tca gag gat ctg ctc ttg gtc aca gac cct gct ttt ctg tct tgc Asn Ser Glu Asp Leu Leu Leu Val Thr Asp Pro Ala Phe Leu Ser Cys 415 420 425	1420
ggc tgt gtc tca ggt agt ggt ctc agg ctt gga ggc tcc cca ggc agc Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser 430 435 440	1468
cta ctg gac agg ttg agg ctg tca ttt gca aag gaa ggg gac tgg aca Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Gly Asp Trp Thr 445 450 455	1516
gca gac cca acc tgg aga act ggg tcc cca gga ggg ggc tct gag agt Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser 460 465 470	1564
gaa gca ggt tcc ccc cct ggt ctg gac atg gac aca ttt gac agt ggc	1612

Glu Ala Gly Ser Pro Pro Gly Leu Asp Met Asp Thr Phe Asp Ser Gly  
 475 480 485 490

ttt gca ggt tca gac tgt ggc agc ccc gtg gag act gat gaa gga ccc 1660  
 Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu Gly Pro  
 495 500 505

cct cga agc tat ctc cgc cag tgg gtg gtc agg acc cct cca cct gtg 1708  
 Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro Pro Val  
 510 515 520

gac agt gga gcc cag agc agc tagcat 1735  
 Asp Ser Gly Ala Gln Ser Ser  
 525

<210> 12  
 <211> 529  
 <212> PRT  
 <213> mus musculus

<400> 12

Met Pro Arg Gly Pro Val Ala Ala Leu Leu Leu Ile Leu His Gly  
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 Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr  
 20 25 30  
 Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser  
 35 40 45  
 Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe  
 50 55 60  
 Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr  
 65 70 75 80  
 Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val  
 85 90 95  
 Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe  
 100 105 110  
 Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val  
 115 120 125  
 Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu  
 130 135 140  
 Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr  
 145 150 155 160

Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile  
 165 170 175  
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys  
 180 185 190  
 Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr  
 195 200 205  
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln  
 210 215 220  
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu  
 225 230 235 240  
 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile  
 245 250 255  
 His Leu Pro Trp Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr  
 260 265 270  
 Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg Glu His Ser Gly Asn Phe  
 275 280 285  
 Lys Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val  
 290 295 300  
 Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro  
 305 310 315 320  
 Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu  
 325 330 335  
 Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu  
 340 345 350  
 Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro  
 355 360 365  
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly  
 370 375 380  
 Leu Cys Val Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met  
 385 390 395 400  
 Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu  
 405 410 415  
 Leu Val Thr Asp Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser  
 420 425 430  
 Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg  
 435 440 445  
 Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg  
 450 455 460  
 Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro  
 465 470 475 480  
 Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys  
 485 490 495

Gly Ser Pro Val Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg  
                   500                  505                  510  
 Gln Trp Val Val Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser  
                   515                  520                  525  
 Ser

<210> 13  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> WSXWS polypeptide consensus motif

<221> VARIANT  
 <222> (1)...(5)  
 <223> Xaa = Any Amino Acid

<400> 13  
 Trp Ser Xaa Trp Ser  
 1                  5

<210> 14  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Glu-Glu (CEE) Tag amino acid sequence

<400> 14  
 Glu Tyr Met Pro Met Glu  
 1                  5

<210> 15  
 <211> 1701  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> soluble zalpha11R/IgGgamma1 construct

<221> CDS

&lt;222&gt; (1)...(1701)

&lt;400&gt; 15

atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga	48
Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly	
1 5 10 15	
ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg	96
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	
20 25 30	
gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc	144
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr	
35 40 45	
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc	192
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser	
50 55 60	
tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc	240
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr	
65 70 75 80	
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc	288
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val	
85 90 95	
aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt	336
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe	
100 105 110	
ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg	384
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val	
115 120 125	
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac	432
Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp	
130 135 140	
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac	480
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr	
145 150 155 160	

agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile 165 170 175	528
tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys 180 185 190	576
gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser 195 200 205	624
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln 210 215 220	672
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac gct agc acc Thr Gln Ser Glu Glu Lys Glu Gly Trp Asn Pro His Ala Ser Thr 225 230 235 240	720
aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser 245 250 255	768
ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu 260 265 270	816
ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His 275 280 285	864
acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser 290 295 300	912
gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys 305 310 315 320	960
aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag	1008

Asn Val	Asn His	Lys Pro	Ser Asn	Thr Lys	Val Asp	Lys Lys	Val Glu	
	325			330			335	
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct								1056
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	340			345			350	
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag								1104
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	355			360			365	
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg								1152
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	370			375			380	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac								1200
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	385			390			395	400
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac								1248
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	405			410			415	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac								1296
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	420			425			430	
tgg ctg aat gcc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc								1344
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	435			440			445	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga								1392
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	450			455			460	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag								1440
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	465			470			475	480
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac								1488
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	485			490			495	

atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag 1536  
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 500 505 510

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc 1584  
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 515 520 525

aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca 1632  
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 530 535 540

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc 1680  
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 545 550 555 560

ctc tcc ctg tct ccg ggt aaa 1701  
 Leu Ser Leu Ser Pro Gly Lys  
 565

<210> 16

<211> 567

<212> PRT

<213> Artificial Sequence

<400> 16

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly  
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 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr  
 20 25 30  
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr  
 35 40 45  
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser  
 50 55 60  
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr  
 65 70 75 80  
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val  
 85 90 95  
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe  
 100 105 110  
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val  
 115 120 125



Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp
130						135					140				
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
145					150					155					160
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile
				165					170					175	
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Pro	Leu	Glu	Phe	Arg	Lys	
		180					185					190			
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser
		195					200				205				
Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
	210					215					220				
Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Ala	Ser	Thr
225					230					235					240
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser
				245					250					255	
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
		260						265					270		
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
		275				280						285			
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
	290					295					300				
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys
305					310					315					320
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu
				325					330					335	
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro
		340						345					350		
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
		355					360					365			
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
	370					375					380				
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp
				390						395					400
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr
				405					410					415	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
			420					425					430		
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu
		435					440					445			
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
	450					455					460				

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
 465 470 475 480  
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 485 490 495  
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 500 505 510  
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 515 520 525  
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 530 535 540  
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 545 550 555 560  
 Leu Ser Leu Ser Pro Gly Lys  
 565

&lt;210&gt; 17

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; soluble human IL-2Rgamma/human kappa light chain construct

&lt;221&gt; CDS

&lt;222&gt; (1)...(1083)

&lt;400&gt; 17

atg ttg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg 48  
 Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu

1 5 10 15

ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg 96  
 Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly

20 25 30

aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac 144  
 Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp

35 40 45

tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg 192

Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val	
50						55					60					
ttc	aat	gtc	gag	tac	atg	aat	tcg	act	tgg	aac	agc	agc	tct	gag	ccc	240
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro	
65					70				75					80		
cag	cct	acc	aac	ctc	act	ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	288
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn	
				85					90					95		
gat	aaa	gtc	cag	aag	tcg	agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	336
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr	
			100					105						110		
tct	ggc	tgt	cag	ttg	caa	aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	384
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe	
		115					120					125				
gtt	gtt	cag	ctc	cag	gac	cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	432
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln	
		130				135					140					
atg	cta	aaa	ctg	cag	aat	ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	480
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu	
145					150					155					160	
aca	ctt	cac	aaa	ctg	agt	gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	528
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn	
				165					170					175		
aga	ttc	ttg	aac	cac	tgt	ttg	gag	cac	ttg	gtg	cag	tac	cgg	act	gac	576
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp	
			180					185					190			
tgg	gac	cac	agc	tgg	act	gaa	caa	tca	gtg	gat	tat	aga	cat	aag	ttc	624
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe	
		195					200					205				
tcc	ttg	cct	agt	gtg	gat	ggg	cag	aaa	cgc	tac	acg	ttt	cgt	gtt	cgg	672
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Thr	Phe	Arg	Val	Arg	
		210				215					220					

agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg 720  
 Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp  
 225 230 235 240  
  
 agc cac cca atc cac tgg ggg agc aat act tca aaa gag aat act gtg 768  
 Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Thr Val  
 245 250 255  
  
 gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 816  
 Ala Ala Pro Ser Val Phe Ile Phe Pro Ser Asp Glu Gln Leu Lys  
 260 265 270  
  
 tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 864  
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
 275 280 285  
  
 gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 912  
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 290 295 300  
  
 tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 960  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
 305 310 315 320  
  
 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 1008  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 325 330 335  
  
 gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 1056  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
 340 345 350  
  
 aag agc ttc aac agg gga gag tgt tag 1083  
 Lys Ser Phe Asn Arg Gly Glu Cys \*  
 355 360

&lt;210&gt; 18

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

Met	Leu	Lys	Pro	Ser	Leu	Pro	Phe	Thr	Ser	Leu	Leu	Phe	Leu	Gln	Leu
1				5					10					15	
Pro	Leu	Leu	Gly	Val	Gly	Leu	Asn	Thr	Thr	Ile	Leu	Thr	Pro	Asn	Gly
			20					25					30		
Asn	Glu	Asp	Thr	Thr	Ala	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp
		35					40					45			
Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val
		50				55					60				
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro
65					70					75				80	
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn
			85						90					95	
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr
			100					105					110		
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe
		115					120					125			
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln
		130			135					140					
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu
145					150					155				160	
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn
			165						170					175	
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp
		180						185					190		
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe
		195					200					205			
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Thr	Phe	Arg	Val	Arg
		210				215					220				
Ser	Arg	Phe	Asn	Pro	Leu	Cys	Gly	Ser	Ala	Gln	His	Trp	Ser	Glu	Trp
225				230						235				240	
Ser	His	Pro	Ile	His	Trp	Gly	Ser	Asn	Thr	Ser	Lys	Glu	Asn	Thr	Val
			245						250					255	
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys
		260						265					270		
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
		275					280					285			
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn
		290				295					300				
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser
305				310						315					320

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
                                   325                                  330                                  335  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
                                   340                                  345                                  350  
 Lys Ser Phe Asn Arg Gly Glu Cys  
                                   355                                  360

<210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC19905

<400> 19  
 acaggatccg ttagcatgcc gcgtggctgg gccgcc 36

<210> 20  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC19906

<400> 20  
 acagaattct tagctggcct ggggtccagg cgt 33

<210> 21  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC19931

<400> 21  
 ggttggtacc gcaagatgcc gcgtggctgg gccgcc 36

<210> 22  
 <211> 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC19932

&lt;400&gt; 22

cggaggatcc gtgagggttc cagccttcc

29

&lt;210&gt; 23

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; FLAG tag amino acid sequence

&lt;400&gt; 23

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

&lt;210&gt; 24

&lt;211&gt; 66

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer spanning vector flanking region and the 5' end of the zalphall

&lt;400&gt; 24

tccactttgc ctttctctcc acaggtgtcc agggaattca tcgataatgc cgcgtggctg  
ggccgc

60

66

&lt;210&gt; 25

&lt;211&gt; 699

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag  
ggggcacctg cagctttcct cttccccca aaaccaagg acacctcat gatctcccg  
acctctgagg tcacatgcgt ggtggtggac gtgagccacg aagacctga ggtcaagttc

60

120

180

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aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacagggtg acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt ctctctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

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<210> 26

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> First Oligonucleotide primer spanning 3' end of  
the zalphall extracellular domain and the 5' end  
of Fc4

<400> 26

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gcacggtggg catgtgtgag ttttgtctga agatctgggc tcgtgagggt tccagccttc 60
ct 62

```

<210> 27

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Second Oligonucleotide primer spanning 3' end of  
the zalphall extracellular domain and the 5' end  
of Fc4

<400> 27

```

agaccagtc agaggagtta aaggaaggct ggaaccctca cgagcccaga tcttcagaca 60
a 61

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<210> 28

<211> 67

<212> DNA

<213> Artificial Sequence



&lt;220&gt;

<223> Oligonucleotide primer spanning the 3' end of Fc4  
and the vector flanking region

&lt;400&gt; 28

gtgggcctct	ggggtgggta	caacccaga	gctgttttaa	tctagattat	ttacccgag	60
acagga						67

&lt;210&gt; 29

&lt;211&gt; 1821

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Polynucleotide encoding MBP-human  $\alpha$ 1 soluble  
receptor fusion

&lt;221&gt; CDS

&lt;222&gt; (1)...(1821)

&lt;400&gt; 29

atg	aaa	atc	gaa	gaa	ggt	aaa	ctg	gta	atc	tgg	att	aac	ggc	gat	aaa	48
Met	Lys	Ile	Glu	Glu	Gly	Lys	Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	
1			5					10					15			

ggc	tat	aac	ggt	ctc	gct	gaa	gtc	ggt	aag	aaa	ttc	gag	aaa	gat	acc	96
Gly	Tyr	Asn	Gly	Leu	Ala	Glu	Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	
			20				25					30				

gga	att	aaa	gtc	acc	gtt	gag	cat	ccg	gat	aaa	ctg	gaa	gag	aaa	ttc	144
Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	
		35				40						45				

cca	cag	gtt	gcg	gca	act	ggc	gat	ggc	cct	gac	att	atc	ttc	tgg	gca	192
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	
		50				55						60				

cac	gac	cgc	ttt	ggt	ggc	tac	gct	caa	tct	ggc	ctg	ttg	gct	gaa	atc	240
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	
		65				70					75				80	

acc	ccg	gac	aaa	gcg	ttc	cag	gac	aag	ctg	tat	ccg	ttt	acc	tgg	gat	288
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp	
85 90 95	
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa	336
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu	
100 105 110	
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa	384
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys	
115 120 125	
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt	432
Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly	
130 135 140	
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg	480
Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro	
145 150 155 160	
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag	528
Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys	
165 170 175	
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt	576
Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly	
180 185 190	
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac	624
Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp	
195 200 205	
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg	672
Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala	
210 215 220	
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa	720
Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys	
225 230 235 240	
gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc	768
Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser	
245 250 255	

aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Gly Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln 385 390 395 400	1200
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu 405 410 415	1248
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc	1296

Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr	
420 425 430	
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac	1344
Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr	
435 440 445	
acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt	1392
Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser	
450 455 460	
gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc	1440
Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser	
465 470 475 480	
ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act	1488
Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr	
485 490 495	
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa	1536
Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu	
500 505 510	
gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag	1584
Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln	
515 520 525	
tac agg aac ccg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg	1632
Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu	
530 535 540	
atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc	1680
Ile Ser Val Asp Ser Arg Ser Val Ser Leu Pro Leu Glu Phe Arg	
545 550 555 560	
aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc	1728
Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly	
565 570 575	
tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt	1776
Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe	
580 585 590	

cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac tag 1821  
 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His \*  
 595 600 605

<210> 30  
 <211> 606  
 <212> PRT  
 <213> Artificial Sequence

<400> 30  
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys  
 1 5 10 15  
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr  
 20 25 30  
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
 35 40 45  
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
 50 55 60  
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile  
 65 70 75 80  
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp  
 85 90 95  
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu  
 100 105 110  
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys  
 115 120 125  
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly  
 130 135 140  
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro  
 145 150 155 160  
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys  
 165 170 175  
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly  
 180 185 190  
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
 195 200 205  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
 210 215 220  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
 225 230 235 240  
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser  
 245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
 260 265 270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
 275 280 285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
 290 295 300  
 Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
 305 310 315 320  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
 325 330 335  
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala  
 340 345 350  
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
 355 360 365  
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val  
 370 375 380  
 Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln  
 385 390 395 400  
 Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu  
 405 410 415  
 Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr  
 420 425 430  
 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr  
 435 440 445  
 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser  
 450 455 460  
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser  
 465 470 475 480  
 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr  
 485 490 495  
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu  
 500 505 510  
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 515 520 525  
 Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu  
 530 535 540  
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg  
 545 550 555 560  
 Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly  
 565 570 575  
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 595 600 605

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21

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<223> Zalpha11 TaqMan Probe, ZG31

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23

<210> 43

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<212> DNA

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<223> Oligonucleotide primer, rRNA forward primer

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<210> 44

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<223> Oligonucleotide primer, rRNA reverse primer

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18

<210> 45

<211> 22

<212> DNA

<213> Artificial Sequence

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&lt;223&gt; rRNA TaqMan probe

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22

&lt;210&gt; 46

&lt;211&gt; 3072

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54)...(491)

&lt;400&gt; 46

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56

Met

1

gag agg acc ctt gtc tgt ctg gta gtc atc ttc ttg ggg aca gtg gcc

104

Glu Arg Thr Leu Val Cys Leu Val Val Ile Phe Leu Gly Thr Val Ala

5

10

15

cat aaa tca agc ccc caa ggg cca gat cgc ctc ctg att aga ctt cgt

152

His Lys Ser Ser Pro Gln Gly Pro Asp Arg Leu Leu Ile Arg Leu Arg

20

25

30

cac ctt att gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg

200

His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu

35

40

45

gat cct gaa ctt cta tca gct cca caa gat gta aag ggg cac tgt gag

248

Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu

50

55

60

65

cat gca gct ttt gcc tgt ttt cag aag gcc aaa ctc aag cca tca aac

296

His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn

70

75

80

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344

Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg

85

90

95

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Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe	
115 120 125	
cta gaa aga cta aaa tgg ctc ctt caa aag atg att cat cag cat ctc	488
Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu	
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&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 47

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35 40 45
Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys
50 55 60
Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
65 70 75 80
Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
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Arg Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile
100 105 110
Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
115 120 125
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<210> 56

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41

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<213> Artificial Sequence



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&lt;400&gt; 59

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&lt;210&gt; 60

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;210&gt; 61

&lt;211&gt; 43

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC23656

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&lt;210&gt; 62

&lt;211&gt; 20

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48

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Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro  
20 25 30

96

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35 40 45

144

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50 55 60

192

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65 70 75 80

240

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Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln  
85 90 95

288

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336

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Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu	
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Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn	
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Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln	
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 Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu  
 545 550 555 560

tcg agc cct gga ccc cag gcc agc taa 1707  
 Ser Ser Pro Gly Pro Gln Ala Ser \*  
 565

<210> 65

<211> 568

<212> PRT

<213> homo sapiens

<400> 65

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly  
 1 5 10 15  
 Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro  
 20 25 30

Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp  
 35 40 45  
 Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu  
 50 55 60  
 Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser  
 65 70 75 80  
 Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln  
 85 90 95  
 Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His  
 100 105 110  
 Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp  
 115 120 125  
 Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp  
 130 135 140  
 Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu  
 145 150 155 160  
 Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala  
 165 170 175  
 Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn  
 180 185 190  
 Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val  
 195 200 205  
 Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser  
 210 215 220  
 Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr  
 225 230 235 240  
 Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln  
 245 250 255  
 Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu  
 260 265 270  
 Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His  
 275 280 285  
 Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu  
 290 295 300  
 Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys  
 305 310 315 320  
 Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp  
 325 330 335  
 Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro  
 340 345 350  
 Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala  
 355 360 365

Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr  
 370 375 380  
 Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Arg Asp Arg Pro  
 385 390 395 400  
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly  
 405 410 415  
 Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu  
 420 425 430  
 Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu  
 435 440 445  
 Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly  
 450 455 460  
 Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys  
 465 470 475 480  
 Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly  
 485 490 495  
 Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu  
 500 505 510  
 Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp  
 515 520 525  
 Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly  
 530 535 540  
 Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu  
 545 550 555 560  
 Ser Ser Pro Gly Pro Gln Ala Ser  
 565

&lt;210&gt; 66

&lt;211&gt; 741

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Degenerate polynucleotide sequence of SEQ ID NO:69

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(741)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 66

atggarmgna aryntgyws nccnaarccn ccncnacna argcnwsnyt nccnacngay  
 ccncnggnt gggngtygcc ngaytyngtn tgytayacng aytayytnc racngtnath

60

120

```
<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence
```

<223> WXXW motif

$\langle 222 \rangle$  (1)...(4)

<223> Xaa = Any Amino Acid

Trp Xaa Xaa Trp

1

<211> 741

<213> Homo sapiens

<221> CDS

&lt;222&gt; (1)...(741)

atg gag agg aag ctc tgc agt ccc aag cca ccc ccc acc aag gcc tct 48  
Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser  
1 5 10 15

ctc ccc act gac cct cca ggc tgg ggc tgc ccc gac ctc gtc tgc tac 96



Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	
			20					25					30			
acc	gat	tac	ctc	cag	acg	gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	144
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	
		35					40					45				
cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	ata	ctt	tct	aat	aat	act	ggg	192
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly	
		50					55				60					
tgc	tat	atc	aag	gac	aga	aca	ctg	gac	ctc	agg	caa	gac	cag	tat	gaa	240
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu	
		65				70				75					80	
gag	ctg	aag	gac	gag	gcc	acc	tcc	tgc	agc	ctc	cac	agg	tgc	gcc	cac	288
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	
					85					90					95	
aat	gcc	acg	cat	gcc	acc	tac	acc	tgc	cac	atg	gat	gta	ttc	cac	ttc	336
Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	
			100					105						110		
atg	gcc	gac	gac	att	ttc	agt	gtc	aac	atc	aca	gac	cag	tct	ggc	aac	384
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	
		115					120					125				
tac	tcc	cag	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	gag	agc	aga	cag	tat	432
Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Arg	Gln	Tyr	
		130				135					140					
aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	cct	gcc	ttc	tac	atg	ctg	480
Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe	Tyr	Met	Leu	
		145				150				155					160	
aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac	agg	aac	cgg	gga	gac	ccc	528
Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg	Gly	Asp	Pro	
			165						170					175		
tgg	gct	gtg	agt	cgg	agg	aga	aag	ctg	atc	tca	gtg	gac	tca	aga	agt	576
Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Ser	
			180					185						190		

gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc tat gag ctg 624  
 Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu  
 195 200 205

cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag ggg acc tgg 672  
 Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp  
 210 215 220

agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca gag gag tta 720  
 Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu  
 225 230 235 240

aag gaa ggc tgg aac cct cac 741  
 Lys Glu Gly Trp Asn Pro His  
 245

<210> 69

<211> 247

<212> PRT

<213> Homo sapiens

<400> 69

Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser  
 1 5 10 15  
 Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr  
 20 25 30  
 Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu  
 35 40 45  
 His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly  
 50 55 60  
 Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu  
 65 70 75 80  
 Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His  
 85 90 95  
 Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe  
 100 105 110  
 Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn  
 115 120 125  
 Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Arg Gln Tyr  
 130 135 140  
 Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu  
 145 150 155 160

```

Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro
      165              170              175
Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser
      180              185              190
Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu
      195              200              205
Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp
      210              215              220
Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu
      225              230              235              240
Lys Glu Gly Trp Asn Pro His
      245

```

&lt;210&gt; 70

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Domain linker motif; PAPP motif

&lt;400&gt; 70

Pro Ala Pro Pro

1

&lt;210&gt; 71

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Representative variant soluble receptor with  
domain linker

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(261)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 71

Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser

1

5

10

15

```

Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr
      20      25      30
Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu
      35      40      45
His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly
      50      55      60
Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu
      65      70      75      80
Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His
      85      90      95
Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe
      100      105      110
Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn
      115      120      125
Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Xaa Xaa Pro
      130      135      140
Ala Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gln Tyr Asn Ile
      145      150      155      160
Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly
      165      170      175
Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala
      180      185      190
Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser
      195      200      205
Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val
      210      215      220
Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu
      225      230      235      240
Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu
      245      250      255
Gly Trp Asn Pro His
      260

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<210> 72

<211> 1461

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse zalphall extracellular domain murine  
immunoglobulin gamma 2a heavy chain Fc region  
fusion protein (zalphallm-mG2a) Polynucleotide

&lt;221&gt; CDS

&lt;222&gt; (1)..(1461)

&lt;400&gt; 72

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	

gcc gtc ttc gtt tcg ctc agc cag aaa atc cat gcc gag ttg aga cgc	96
Ala Val Phe Val Ser Leu Ser Gln Lys Ile His Ala Glu Leu Arg Arg	
20 25 30	

ttc cgg aga tgc ctg gac ctc act tgc tac act gac tac ctc tgg acc	144
Phe Arg Arg Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr	
35 40 45	

atc acc tgt gtc ctg gag aca cgg agc ccc aac ccc agc ata ctc agt	192
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser	
50 55 60	

ctc acc tgg caa gat gaa tat gag gaa ctt cag gac caa gag acc ttc	240
Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe	
65 70 75 80	

tgc agc cta cac agg tct ggc cac aac acc aca cat ata tgg tac acg	288
Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr	
85 90 95	

tgc cat atg cgc ttg tct caa ttc ctg tcc gat gaa gtt ttc att gtc	336
Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val	
100 105 110	

aat gtg acg gac cag tct ggc aac aac tcc caa gag tgt ggc agc ttt	384
Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe	
115 120 125	

gtc ctg gct gag agc atc aaa cca gct ccc ccc ttg aac gtg act gtc	432
Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val	
130 135 140	

gcc ttc tca gga cgc tat gat atc tcc tgg gac tca gct tat gac gaa	480
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Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	Asp	Ser	Ala	Tyr	Asp	Glu	
145					150					155					160	
ccc	tcc	aac	tac	gtg	ctg	agg	ggc	aag	cta	caa	tat	gag	ctg	cag	tat	528
Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	
				165					170					175		
cgg	aac	ctc	aga	gac	ccc	tat	gct	gtg	agg	ccg	gtg	acc	aag	ctg	atc	576
Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile	
			180					185					190			
tca	gtg	gac	tca	aga	aac	gtc	tct	ctt	ctc	cct	gaa	gag	ttc	cac	aaa	624
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys	
			195				200					205				
gat	tct	agc	tac	cag	ctg	cag	gtg	cgg	gca	gcg	cct	cag	cca	ggc	act	672
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr	
			210			215					220					
tca	ttc	agg	ggg	acc	tgg	agt	gag	tgg	agt	gac	ccc	gtc	atc	ttt	cag	720
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln	
				230						235					240	
acc	cag	gct	ggg	gag	ccc	gag	gca	ggc	tgg	gac	cct	cac	gag	ccc	aga	768
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Glu	Pro	Arg	
				245					250					255		
tct	ccc	aca	atc	aag	ccc	tgt	cct	cca	tgc	aaa	tgc	cca	gca	cct	aac	816
Ser	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	
				260				265					270			
ctc	ttg	ggt	gga	cca	tcc	gtc	ttc	atc	ttc	cct	cca	aag	atc	aag	gat	864
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	
			275				280					285				
gta	ctc	atg	atc	tcc	ctg	agc	ccc	ata	gtc	aca	tgt	gtg	gtg	gtg	gat	912
Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	
			290			295					300					
gtg	agc	gag	gat	gac	cca	gat	gtc	cag	atc	agc	tgg	ttt	gtg	aac	aac	960
Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	
				310						315				320		

gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat tac aac Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn 325 330 335	1008
agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp 340 345 350	1056
atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro 355 360 365	1104
gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala 370 375 380	1152
cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met Thr Lys Lys 385 390 395 400	1200
cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile 405 410 415	1248
tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn 420 425 430	1296
act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys 435 440 445	1344
ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys 450 455 460	1392
tca gtg gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe 465 470 475 480	1440
tcc cgg act ccg ggt aaa taa	1461

Ser Arg Thr Pro Gly Lys \*  
485

<210> 73

<211> 486

<212> PRT

<213> Artificial Sequence

<400> 73

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
1				5					10					15	
Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Lys	Ile	His	Ala	Glu	Leu	Arg	Arg
			20				25						30		
Phe	Arg	Arg	Cys	Leu	Asp	Leu	Thr	Cys	Tyr	Thr	Asp	Tyr	Leu	Trp	Thr
		35				40						45			
Ile	Thr	Cys	Val	Leu	Glu	Thr	Arg	Ser	Pro	Asn	Pro	Ser	Ile	Leu	Ser
	50				55					60					
Leu	Thr	Trp	Gln	Asp	Glu	Tyr	Glu	Glu	Leu	Gln	Asp	Gln	Glu	Thr	Phe
65				70					75					80	
Cys	Ser	Leu	His	Arg	Ser	Gly	His	Asn	Thr	Thr	His	Ile	Trp	Tyr	Thr
			85					90					95		
Cys	His	Met	Arg	Leu	Ser	Gln	Phe	Leu	Ser	Asp	Glu	Val	Phe	Ile	Val
		100					105						110		
Asn	Val	Thr	Asp	Gln	Ser	Gly	Asn	Asn	Ser	Gln	Glu	Cys	Gly	Ser	Phe
	115					120						125			
Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Leu	Asn	Val	Thr	Val
	130					135					140				
Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	Asp	Ser	Ala	Tyr	Asp	Glu
145				150					155					160	
Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
		165						170						175	
Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile
		180					185						190		
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys
	195					200						205			
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr
	210				215						220				
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
225				230					235					240	
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Glu	Pro	Arg
		245						250					255		



Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn  
                   260                  265                  270  
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp  
                   275                  280                  285  
 Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp  
                   290                  295                  300  
 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn  
 305                  310                  315                  320  
 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn  
                   325                  330                  335  
 Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp  
                   340                  345                  350  
 Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro  
                   355                  360                  365  
 Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala  
                   370                  375                  380  
 Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys  
 385                  390                  395                  400  
 Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile  
                   405                  410                  415  
 Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn  
                   420                  425                  430  
 Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys  
                   435                  440                  445  
 Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys  
                   450                  455                  460  
 Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe  
 465                  470                  475                  480  
 Ser Arg Thr Pro Gly Lys  
                   485

&lt;210&gt; 74

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC26644

&lt;400&gt; 74

ggggtcgacg gccggccacc atg

<210> 75  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26641

<400> 75  
 caagtgaggt ccaggcatct ccggaagcgt ctcaa 35

<210> 76  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26642

<400> 76  
 ttgagacgct tccggagatg cctggacctc acttg 35

<210> 77  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26662

<400> 77  
 tgtgggagat ctgggctcgt gaggggtccca gcctgc 36

<210> 78  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26643

<400> 78  
 gagcccagat ctcccacaat caagccctgt 30

<210> 79  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC26645

<400> 79  
 aaacgcggcc gcgcatccgg c

21

<210> 80  
 <211> 35  
 <212> PRT  
 <213> Homo sapeins

<400> 80  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15  
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg  
 20 25 30  
 Phe Arg Arg  
 35

<210> 81  
 <211> 966  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(966)

<400> 81  
 ggg ggc ggg ggc gcc gcg cct acg gaa act cag cca cct gtg aca aat  
 Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn  
 1 5 10 15

48

ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata tgg aca tgg aat  
 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn  
 20 25 30

96

cca ccc gag gga gcc agc tca aat tgt agt cta tgg tat ttt agt cat Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His 35 40 45	144
ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa act cgt cgt tca Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser 50 55 60	192
ata gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln 65 70 75 80	240
tgt agc acc aat gag agt gag aag cct agc att ttg gtt gaa aaa tgc Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys 85 90 95	288
atc tca ccc cca gaa ggt gat cct gag tct gct gtg act gag ctt caa Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln 100 105 110	336
tgc att tgg cac aac ctg agc tac atg aag tgt tct tgg ctc cct gga Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly 115 120 125	384
agg aat acc agt ccc gac act aac tat act ctc tac tat tgg cac aga Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg 130 135 140	432
agc ctg gaa aaa att cat caa tgt gaa aac atc ttt aga gaa ggc caa Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln 145 150 155 160	480
tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag gat tcc agt ttt Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe 165 170 175	528
gaa caa cac agt gtc caa ata atg gtc aag gat aat gca gga aaa att Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile 180 185 190	576
aaa cca tcc ttc aat ata gtg cct tta act tcc cgt gtg aaa cct gat Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp 195 200 205	624

cct cca cat att aaa aac ctc tcc ttc cac aat gat gac cta tat gtg 672  
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Leu Tyr Val  
 210 215 220  
  
 caa tgg gag aat cca cag aat ttt att agc aga tgc cta ttt tat gaa 720  
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu  
 225 230 235 240  
  
 gta gaa gtc aat aac agc caa act gag aca cat aat gtt ttc tac gtc 768  
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val  
 245 250 255  
  
 caa gag gct aaa tgt gag aat cca gaa ttt gag aga aat gtg gag aat 816  
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn  
 260 265 270  
  
 aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat act ttg aac aca 864  
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr  
 275 280 285  
  
 gtc aga ata aga gtc aaa aca aat aag tta tgc tat gag gat gac aaa 912  
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys  
 290 295 300  
  
 ctc tgg agt aat tgg agc caa gaa atg agt ata ggt aag aag cgc aat 960  
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn  
 305 310 315 320  
  
 tcc aca 966  
 Ser Thr

&lt;210&gt; 82

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 82

Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn  
 1 5 10 15  
 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn  
 20 25 30

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His  
 35 40 45  
 Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser  
 50 55 60  
 Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln  
 65 70 75 80  
 Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys  
 85 90 95  
 Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln  
 100 105 110  
 Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly  
 115 120 125  
 Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg  
 130 135 140  
 Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln  
 145 150 155 160  
 Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe  
 165 170 175  
 Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile  
 180 185 190  
 Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp  
 195 200 205  
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val  
 210 215 220  
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu  
 225 230 235 240  
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val  
 245 250 255  
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn  
 260 265 270  
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr  
 275 280 285  
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys  
 290 295 300  
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn  
 305 310 315 320  
 Ser Thr

&lt;210&gt; 83

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(951)

&lt;400&gt; 83

gac acc gag ata aaa gtt aac cct cct cag gat ttt gag ata gtg gat	48
Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp	
1 5 10 15	

ccc gga tac tta ggt tat ctc tat ttg caa tgg caa ccc cca ctg tct	96
Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser	
20 25 30	

ctg gat cat ttt aag gaa tgc aca gtg gaa tat gaa cta aaa tac cga	144
Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg	
35 40 45	

aac att ggt agt gaa aca tgg aag acc atc att act aag aat cta cat	192
Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His	
50 55 60	

tac aaa gat ggg ttt gat ctt aac aag ggc att gaa gcg aag ata cac	240
Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His	
65 70 75 80	

acg ctt tta cca tgg caa tgc aca aat gga tca gaa gtt caa agt tcc	288
Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser	
85 90 95	

tgg gca gaa act act tat tgg ata tca cca caa gga att cca gaa act	336
Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr	
100 105 110	

aaa gtt cag gat atg gat tgc gta tat tac aat tgg caa tat tta ctc	384
Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu	
115 120 125	

tgt tct tgg aaa cct ggc ata ggt gta ctt ctt gat acc aat tac aac	432
Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn	
130 135 140	

ttg ttt tac tgg tat gag ggc ttg gat cat gca tta cag tgt gtt gat	480
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Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ala Leu Gln Cys Val Asp	
145 150 155 160	
tac atc aag gct gat gga caa aat ata gga tgc aga ttt ccc tat ttg	528
Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu	
165 170 175	
gag gca tca gac tat aaa gat ttc tat att tgt gtt aat gga tca tca	576
Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser	
180 185 190	
gag aac aag cct atc aga tcc agt tat ttc act ttt cag ctt caa aat	624
Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn	
195 200 205	
ata gtt aaa cct ttg ccg cca gtc tat ctt act ttt act cgg gag agt	672
Ile Val Lys Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser	
210 215 220	
tca tgt gaa att aag ctg aaa tgg agc ata cct ttg gga cct att cca	720
Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro	
225 230 235 240	
gca agg tgt ttt gat tat gaa att gag atc aga gaa gat gat act acc	768
Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr	
245 250 255	
ttg gtg act gct aca gtt gaa aat gaa aca tac acc ttg aaa aca aca	816
Leu Val Thr Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr	
260 265 270	
aat gaa acc cga caa tta tgc ttt gta gta aga agc aaa gtg aat att	864
Asn Glu Thr Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile	
275 280 285	
tat tgc tca gat gac gga att tgg agt gag tgg agt gat aaa caa tgc	912
Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys	
290 295 300	
tgg gaa ggt gaa gac cta tcg aag aaa act ttg cta cgt	951
Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg	
305 310 315	



<210> 84  
 <211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Asp	Thr	Glu	Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp
1				5					10					15	
Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser
		20						25					30		
Leu	Asp	His	Phe	Lys	Glu	Cys	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg
		35					40					45			
Asn	Ile	Gly	Ser	Glu	Thr	Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His
	50					55					60				
Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His
	65				70					75				80	
Thr	Leu	Leu	Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser
				85					90					95	
Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr
			100					105					110		
Lys	Val	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu
		115					120					125			
Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn
		130				135					140				
Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp
	145				150					155				160	
Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu
			165						170					175	
Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser
			180				185						190		
Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn
		195					200					205			
Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser
	210					215						220			
Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro
	225				230					235				240	
Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr
			245						250					255	
Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr
			260					265					270		
Asn	Glu	Thr	Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile
		275					280						285		

Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys  
 290 295 300  
 Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg  
 305 310 315

<210> 85  
 <211> 519  
 <212> DNA  
 <213> Homo sapeins

<220>  
 <221> CDS  
 <222> (1)...(519)

<400> 85

atc acg tgc cct ccc ccc atg tcc gtg gaa cac gca gac atc tgg gtc 48  
 Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val  
 1 5 10 15

aag agc tac agc ttg tac tcc agg gag cgg tac att tgt aac tct ggt 96  
 Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly  
 20 25 30

ttc aag cgt aaa gcc gcc acg tcc agc ctg acg gag tgc gtg ttg aac 144  
 Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn  
 35 40 45

aag gcc acg aat gtc gcc cac tgg aca acc ccc agt ctc aaa tgc att 192  
 Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile  
 50 55 60

aga gac cct gcc ctg gtt cac caa agg cca gcg cca ccc tcc aca gta 240  
 Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val  
 65 70 75 80

acg acg gca ggg gtg acc cca cag cca gag agc ctc tcc cct tct gga 288  
 Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly  
 85 90 95

aaa gag ccc gca gct tca tct ccc agc tca aac aac aca gcg gcc aca 336  
 Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr  
 100 105 110

aca gca gct att gtc ccg ggc tcc cag ctg atg cct tca aaa tca cct 384  
 Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro  
 115 120 125

tcc aca gga acc aca gag ata agc agt cat gag tcc tcc cac ggc acc 432  
 Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr  
 130 135 140

ccc tct cag aca aca gcc aag aac tgg gaa ctc aca gca tcc gcc tcc 480  
 Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser  
 145 150 155 160

cac cag ccg cca ggt gtg tat cca cag ggc cac agc gac 519  
 His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp  
 165 170

<210> 86

<211> 173

<212> PRT

<213> Homo sapeins

<400> 86

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val  
 1 5 10 15  
 Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly  
 20 25 30  
 Phe Lys Arg Lys Ala Gly Thr Ser Leu Thr Glu Cys Val Leu Asn  
 35 40 45  
 Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile  
 50 55 60  
 Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val  
 65 70 75 80  
 Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly  
 85 90 95  
 Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr  
 100 105 110  
 Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro  
 115 120 125  
 Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr  
 130 135 140  
 Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser  
 145 150 155 160

His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp  
 165 170

165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995